RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/018,105

DATE: 01/09/2002
TIME: 13:56:27

Input Set : A:\10182015999.txt
Output Set: N:\CRF3\01082002\J018105.raw

p.5

ENTERED

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 4 <110> APPLICANT: ROEMER, Terry
 5        BUSSEY, Howard
 6        DAVISON, John
 8 <120> TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
 9        SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
10        DISCOVERY
12 <130> FILE REFERENCE: 10182-015
14 <140> CURRENT APPLICATION NUMBER: US/10/018,105
15 <141> CURRENT FILING DATE: 2001-11-05
17 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00533
18 <151> PRIOR FILING DATE: 2000-05-05
20 <150> PRIOR APPLICATION NUMBER: 60/132,878
21 <151> PRIOR FILING DATE: 1999-05-05
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 7558
29 <212> TYPE: DNA
30 <213> ORGANISM: Candida albicans
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (2770)..(7110)
36 <400> SEQUENCE: 1
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41 gtgtaccctg tattgatcgt ggaggatgtc gagctccaca actgcacgtg ggagtttccg 180
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51 cttgcaaggg aaggcgcata caacctatcg cattggtttg gaaagttgcc gacaaaacag 480
53 tacgttgcgg gtactagaca tgcaggtgga ttacgaagct cgtgaccggg agagagcatt 540
55 gaaggaggcc aatagatact ttccattcct tgatgtgaag atacatagac cataaaagca 600
57 caaggctgcg aaatatatac gcgtatagac tctactaata aacatccaaa ccagagtgaa 660
59 aaaaaaaaat acaacacaaa ccagaaaaaa aacaaacgaa ccacttacaa gacccatctc 720
61 taccacaaca ccaatgtact gggtgctact ccttttcgtg tcgatatgca tggccaacac 780
63 ggagacatgc ttggtacggg tgcccgagta ctacaatatt gtaccgcacc cgtcacccat 840
65 atccagggat gccaggttca gtcgcgagct ccatcgtctc aacaccaccc acacagtact 900
67 actagactac cccattggat ctatcgacga ccaggatatg tccaacataa tcacagtcac 960
69 atacgatacc gttgcgcaac cacgatcaac actactagtg cgcgtgaaca actacggaga 1020
71 caatacgttt acgaacggcg acatgctcaa cattaagcta tgctggccgg ccaccatgcc 1080
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81 cacaatattc attgtctgga acatcttgcc atatttggtt aagggtgtat tagaagccgt 1380
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RAW SEQUENCE LISTING
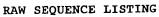PATENT APPLICATION: US/10/018,105

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 95 tcggggcctt gaaacgtttt tcagatgaag cttatgcgaa gtctttgctc tatgatgcag 1800
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 99 tgtatcctga taaggcggaa ctatggggcc taaatgtcaa tcacggacaa aagatatacc 1920
101 taaggttaag agaacatcac aatgataaac tgtttctccc catgggtgat atagtaggga 1980
103 ccttacttca tgaattaaca cacaatttgt atagtgctca cgatagtaag ttctacaagt 2040
105 ttttggacaa actaaagtcg agatacgacg acatacattg taggggagcc aaaacaaaat 2100
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117 gtcctacaga aggtaaacca gttggaacat ttgctaatga tatcattgat ttaacatcgg 2460
119 acactgaaga aactccaatt caacctgata acccgaaacg ccgcatactc cacgagataa 2520
121 ttgatttaac ttcagataca gaagacatag agccaacatc accagaggta atatgtatag 2580
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125 ctcgtgcaag gattaagcac cgaaaaaaaa tatgtggatg cgttgttatt agttttactc 2700
127 tttgcttttt ctgaaaagaa acattaacgt gttctactag tttgtcacac tacgacacaa 2760
129 gtccttgaa atg tca ttt gca agg tat atc tac tac acc att gcg gtt gct 2811
130             Met Ser Phe Ala Arg Tyr Ile Tyr Tyr Thr Ile Ala Val Ala
131              1               5                  10
133 gtt tta tta aat ttt gtc aaa gct act gaa aat aac aat ttt aaa ctt     2859
134 Val Leu Leu Asn Phe Val Lys Ala Thr Glu Asn Asn Asn Phe Lys Leu
135  15                  20                  25                  30
137 gaa gtt gaa gcg tca tgg agc aat att gat ttc ctt cct agc ttt ata     2907
138 Glu Val Glu Ala Ser Trp Ser Asn Ile Asp Phe Leu Pro Ser Phe Ile
139                  35                  40                  45
141 gag gcc atc gtt ggc ttc aat gac tct ttg tac gaa cag aca att gaa     2955
142 Glu Ala Ile Val Gly Phe Asn Asp Ser Leu Tyr Glu Gln Thr Ile Glu
143                  50                  55                  60
145 aca att ttt ggt tta gga gac act gaa gtg gaa tta gaa gat gat gct     3003
146 Thr Ile Phe Gly Leu Gly Asp Thr Glu Val Glu Leu Glu Asp Asp Ala
147              65                  70                  75
149 tca gat caa gaa ata tat tct acc gtg atc aac tca tta ggg tta aca     3051
150 Ser Asp Gln Glu Ile Tyr Ser Thr Val Ile Asn Ser Leu Gly Leu Thr
151          80                  85                  90
153 gat caa gat ttg gat ttt att aat ttt gat tta acc aac aaa aaa cat     3099
154 Asp Gln Asp Leu Asp Phe Ile Asn Phe Asp Leu Thr Asn Lys Lys His
155  95                  100                 105                 110
157 aca cca aga atc gca gcc cat tac gat cac tat tct gat gtt cta act     3147
158 Thr Pro Arg Ile Ala Ala His Tyr Asp His Tyr Ser Asp Val Leu Thr
159                  115                 120                 125
161 aag ttt ggc gat cga ctc aaa agt gaa tgt gca aaa gac tct ttt ggg     3195
162 Lys Phe Gly Asp Arg Leu Lys Ser Glu Cys Ala Lys Asp Ser Phe Gly
163              130                 135                 140
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165 aat gca gtg gaa acg aaa aat ggt caa att caa acg tgg tta cta tat   3243
166 Asn Ala Val Glu Thr Lys Asn Gly Gln Ile Gln Thr Trp Leu Leu Tyr
167         145                 150                 155
169 aac gat aag ata tat tgt tcg gct aat gat ttg ttt gca tta cga act   3291
170 Asn Asp Lys Ile Tyr Cys Ser Ala Asn Asp Leu Phe Ala Leu Arg Thr
171         160                 165                 170
173 gat ttg agt tct cat tct aca ctt tta ttt gat agg att att gga aaa   3339
174 Asp Leu Ser Ser His Ser Thr Leu Leu Phe Asp Arg Ile Ile Gly Lys
175 175                 180                 185                 190
177 tca aaa gat gca cct ttg gtg att tta tat gga agc ccg act gag gaa   3387
178 Ser Lys Asp Ala Pro Leu Val Ile Leu Tyr Gly Ser Pro Thr Glu Glu
179                 195                 200                 205
181 ctg act aaa gat ttt ctt aaa ata ttg tat cca gat gca aag gct gga   3435
182 Leu Thr Lys Asp Phe Leu Lys Ile Leu Tyr Pro Asp Ala Lys Ala Gly
183         210                 215                 220
185 aaa tta aag ttt gta tgg agg tac att cca ctg gga atc aaa aaa ctg   3483
186 Lys Leu Lys Phe Val Trp Arg Tyr Ile Pro Leu Gly Ile Lys Lys Leu
187         225                 230                 235
189 gac tca att tct gga tac ggt gta tca ttg aaa atg gaa aag tat gat   3531
190 Asp Ser Ile Ser Gly Tyr Gly Val Ser Leu Lys Met Glu Lys Tyr Asp
191         240                 245                 250
193 tat tct ggt gca gaa gga aat cca aag tat gat ttg agt cga gat ttc   3579
194 Tyr Ser Gly Ala Glu Gly Asn Pro Lys Tyr Asp Leu Ser Arg Asp Phe
195 255                 260                 265                 270
197 acc aga att aat gac tcg caa gag ttg gtc ctg gtc aat gaa aaa cat   3627
198 Thr Arg Ile Asn Asp Ser Gln Glu Leu Val Leu Val Asn Glu Lys His
199                 275                 280                 285
201 tcg tat gaa ctt ggt gtt aaa ttg act tca ttc ata tta tcc aat cgt   3675
202 Ser Tyr Glu Leu Gly Val Lys Leu Thr Ser Phe Ile Leu Ser Asn Arg
203         290                 295                 300
205 tac aag agt act aaa tat gac ctt tta gat acg att tta acc aac ttt   3723
206 Tyr Lys Ser Thr Lys Tyr Asp Leu Leu Asp Thr Ile Leu Thr Asn Phe
207         305                 310                 315
209 ccc aag ttt att cct tac att gca cga tta cca aaa tta cta aat cat   3771
210 Pro Lys Phe Ile Pro Tyr Ile Ala Arg Leu Pro Lys Leu Leu Asn His
211         320                 325                 330
213 gaa aaa gtt aaa tcc aaa gtg ctt gga aat gaa gat ata ggg cta tct   3819
214 Glu Lys Val Lys Ser Lys Val Leu Gly Asn Glu Asp Ile Gly Leu Ser
215 335                 340                 345                 350
217 caa gac tcc tac gga ata tat atc aac ggt tcc cca ata aat cca cta   3867
218 Gln Asp Ser Tyr Gly Ile Tyr Ile Asn Gly Ser Pro Ile Asn Pro Leu
219                 355                 360                 365
221 gag tta gat att tac aat cta ggt acc agg ata aag gag gaa tta cag   3915
222 Glu Leu Asp Ile Tyr Asn Leu Gly Thr Arg Ile Lys Glu Glu Leu Gln
223                 370                 375                 380
225 act gtg aaa gat tta gtg aaa ctt gga ttt gat acc gta caa gca aag   3963
226 Thr Val Lys Asp Leu Val Lys Leu Gly Phe Asp Thr Val Gln Ala Lys
227         385                 390                 395
229 ctc ttg ata gca aaa ttt gct tta ctt tca gct gtt aaa caa aca caa   4011
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230 Leu Leu Ile Ala Lys Phe Ala Leu Leu Ser Ala Val Lys Gln Thr Gln
231     400             405             410
233 ttt cga aat ggg aat aca tta atg ggt aac aat gaa aat aga ttt aaa   4059
234 Phe Arg Asn Gly Asn Thr Leu Met Gly Asn Asn Glu Asn Arg Phe Lys
235 415             420             425             430
237 gtg tat gaa aat gaa ttt aag aag ggt agt tca gaa aag ggt ggg gtc   4107
238 Val Tyr Glu Asn Glu Phe Lys Lys Gly Ser Ser Glu Lys Gly Gly Val
239             435             440             445
241 ttg ttt ttc aat aac att gaa tta gac aac aca ttc aag gag tac acc   4155
242 Leu Phe Phe Asn Asn Ile Glu Leu Asp Asn Thr Phe Lys Glu Tyr Thr
243             450             455             460
245 act gat cgt gag gag gca tat tta gga gtt ggt tct cat aaa ctt aag   4203
246 Thr Asp Arg Glu Glu Ala Tyr Leu Gly Val Gly Ser His Lys Leu Lys
247         465             470             475
249 cca aat caa att ccg tta ttg aaa gag aac atc cat gat tta att ttc   4251
250 Pro Asn Gln Ile Pro Leu Leu Lys Glu Asn Ile His Asp Leu Ile Phe
251     480             485             490
253 gca tta aat ttt ggg aac aaa aac caa ttg cgg gtg ttt ttc act tta   4299
254 Ala Leu Asn Phe Gly Asn Lys Asn Gln Leu Arg Val Phe Phe Thr Leu
255 495             500             505             510
257 tct aag gtg att ttg gac tcc ggt ata cct caa caa gtt gga gtt ttg   4347
258 Ser Lys Val Ile Leu Asp Ser Gly Ile Pro Gln Gln Val Gly Val Leu
259             515             520             525
261 ccc gtt ata gga gat gac cca atg gat ctg tta ctc gct gag aaa ttt   4395
262 Pro Val Ile Gly Asp Asp Pro Met Asp Leu Leu Leu Ala Glu Lys Phe
263             530             535             540
265 tat tgg att gct gag aaa tca agc aca caa gag gca tta gca ata ttg   4443
266 Tyr Trp Ile Ala Glu Lys Ser Ser Thr Gln Glu Ala Leu Ala Ile Leu
267         545             550             555
269 tat aaa tat ttt gaa tca aac agt cca gat gaa gtt gat gac tta tta   4491
270 Tyr Lys Tyr Phe Glu Ser Asn Ser Pro Asp Glu Val Asp Asp Leu Leu
271     560             565             570
273 gat aaa gtg gaa gta ccc gaa gat tat aaa gtg gat tat aat cat gtg   4539
274 Asp Lys Val Glu Val Pro Glu Asp Tyr Lys Val Asp Tyr Asn His Val
275 575             580             585             590
277 tta aac aag ttt tct ata tca act gct tcg gtc att ttc aat ggg gtt   4587
278 Leu Asn Lys Phe Ser Ile Ser Thr Ala Ser Val Ile Phe Asn Gly Val
279             595             600             605
281 att tac gat tta aga gca cca aac tgg cag att gca atg agt aaa caa   4635
282 Ile Tyr Asp Leu Arg Ala Pro Asn Trp Gln Ile Ala Met Ser Lys Gln
283             610             615             620
285 ata tcc cag gac att tca ctt att aaa act ttc ttg aga cag gga cca   4683
286 Ile Ser Gln Asp Ile Ser Leu Ile Lys Thr Phe Leu Arg Gln Gly Pro
287             625             630             635
289 ata gag ggt aga ttg aaa gat gtt ctt tac tct aat gca aaa tca gaa   4731
290 Ile Glu Gly Arg Leu Lys Asp Val Leu Tyr Ser Asn Ala Lys Ser Glu
291     640             645             650
293 cgc aat tta cgt ata att cca tta gaa cct agt gac att att tac aag   4779
294 Arg Asn Leu Arg Ile Ile Pro Leu Glu Pro Ser Asp Ile Ile Tyr Lys
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295 655                    660                665                670
297 aaa atc gac aag gaa tta ata aac aat tca att gca ttc aag aag cta    4827
298 Lys Ile Asp Lys Glu Leu Ile Asn Asn Ser Ile Ala Phe Lys Lys Leu
299                    675                680                685
301 gat aaa gcg cag ggt gtg tct gga aca ttt tgg cta gtg tcg gat ttt    4875
302 Asp Lys Ala Gln Gly Val Ser Gly Thr Phe Trp Leu Val Ser Asp Phe
303                    690                695                700
305 acc aag tca gca ata att act caa ttg ata gat ttg tta ttg ctt ctc    4923
306 Thr Lys Ser Ala Ile Ile Thr Gln Leu Ile Asp Leu Leu Leu Leu Leu
307                    705                710                715
309 aaa aag aaa gca att cag ata aga att att aat act ggg gat aca gat    4971
310 Lys Lys Lys Ala Ile Gln Ile Arg Ile Ile Asn Thr Gly Asp Thr Asp
311     720                725                730
313 gtt ttt gga aaa ttg aaa aca aag ttt aaa tta acc gcc tta aca aat    5019
314 Val Phe Gly Lys Leu Lys Thr Lys Phe Lys Leu Thr Ala Leu Thr Asn
315 735                740                745                750
317 gga caa att gat gaa att att gag att ttg aaa aaa tcc aac gct tca    5067
318 Gly Gln Ile Asp Glu Ile Ile Glu Ile Leu Lys Lys Ser Asn Ala Ser
319                    755                760                765
321 agt gca aat aat gat gaa ttg aaa aaa atg ctt gag act aag caa tta    5115
322 Ser Ala Asn Asn Asp Glu Leu Lys Lys Met Leu Glu Thr Lys Gln Leu
323                    770                775                780
325 cct gct cat cac tct ttt ttg cta ttc aac tct aga tat ttt aga ttg    5163
326 Pro Ala His His Ser Phe Leu Leu Phe Asn Ser Arg Tyr Phe Arg Leu
327     785                790                795
329 gat gga aat ttt gga tac gag gaa ttg gat caa att ata gag ttt gaa    5211
330 Asp Gly Asn Phe Gly Tyr Glu Glu Leu Asp Gln Ile Ile Glu Phe Glu
331     800                805                810
333 gta tct caa aga ttg aac tta atc ccg gac atc atg gag gca tat ccg    5259
334 Val Ser Gln Arg Leu Asn Leu Ile Pro Asp Ile Met Glu Ala Tyr Pro
335 815                820                825                830
337 gat gag ttt agg tcg aag aag gta agt gat ttt aat ctg gtt ttg tct    5307
338 Asp Glu Phe Arg Ser Lys Lys Val Ser Asp Phe Asn Leu Val Leu Ser
339                    835                840                845
341 gga tta gac aat atg gac tgg ttt gat ttg gtg act tcc ata gtg aca    5355
342 Gly Leu Asp Asn Met Asp Trp Phe Asp Leu Val Thr Ser Ile Val Thr
343                    850                855                860
345 aaa tca ttc cat gtc gac gaa aaa agg ttt att gtt gat gtt aac agg    5403
346 Lys Ser Phe His Val Asp Glu Lys Arg Phe Ile Val Asp Val Asn Arg
347                    865                870                875
349 ttt gat ttt agc tca ttg gat ttt tca aac tcg att gat gta acg act    5451
350 Phe Asp Phe Ser Ser Leu Asp Phe Ser Asn Ser Ile Asp Val Thr Thr
351     880                885                890
353 tat gaa gaa aat agt cca gtt gat gta tta ata att ttg aac cct atg    5499
354 Tyr Glu Glu Asn Ser Pro Val Asp Val Leu Ile Ile Leu Asn Pro Met
355 895                900                905                910
357 gat gaa tat tct caa aaa ttg ata agc ctt gtt aat agc att aca gat    5547
358 Asp Glu Tyr Ser Gln Lys Leu Ile Ser Leu Val Asn Ser Ile Thr Asp
359                    915                920                925
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
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L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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